

## **FIGURE 96**

ATTTC AAGCC CAGCC ATATTTT NTGTT GAACCAACA CAGGAGT CATAAGA ATATTTT NTA  
AAATG GATAG AGAACTG CAAGATG AGTATTG GGTAA TCATTCA AGCCAAGG ACATG ATTGGT  
CAGCC AGGAG CGTTG TNGGAACA CAAGTGT ATTAATTAA ACTTTC AGATGTTA ATGACAA  
TAAGC CTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCGAAACATTTGACATTATT

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# FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGGGACCCCAACCCCGAC  
 CCCAGAGCTTCTCCAGCGGGCGGCAGCGAGCAGGGCTCCCGCGCTTAACCTTCTCTCCGCGGGG  
 CCCAGCCACCTTCCGGGAGTCCGGGTTGCCACCTGCAAACTCTCCGCGCTTCTGCACCTGCCA  
 CCCTTGAGCCAGCGGGGCCCGAGCGAGTCATGGCCAACCGGGGCTGCAGCTGTTGGGC  
 TTCATTCTCGCCTTCTGGGATGGATCGGGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
 GATTCTACTTATGCCGGCGACAACATCGTGACCGCCAGGCCATGACGAGGGGCTGTGGA  
 GTGCTCGGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
 CTGACGACGACATTGCAAGCAACCCGTGCCTTGATGGTGGTCATCCTCTGGGAGTGAT  
 AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCCTGGGAAGCGATGAGGTGC  
 AGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTCTGCAAGTCTGGCTATTTTA  
 GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCATGACCCCTATGACCCCGAT  
 CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
 TTCTGGGAGGTGCCCTACTTTGCTGTTCCTGTCCCGGAAAAACAACCTCTTACCCAACACCA  
 AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAGACTACGTGTGACACAGAGGCAAAAG  
 GAGAAATCATGTTGAAACAACCCGAAAAATGGACATTGAGATACTATCATTAACATTAGGAC  
 CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAACAAACAAACAAAA  
 ACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTATTCTTTCTCTCTCA  
 ATATAGGAGGGAAGATTTTTCATTTGTATTACTGCTTCCCATTTGAGTAATCATACTCAAAAT  
 GGGGGAAGGGGTGCTCTTTAAATATATATAGATATGTATATACATGTTTTCCTATTAAAA  
 ATAGACAGTAAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAAATATCTCTAAAT  
 AGGTAATGTATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC  
 TTATATACATATGTAAACAGTCAAATATCATTTACTCTTCTTATTAGCTTTGGGTGCTCTTG  
 CCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAATTCTTCATGCGTGCCCTTTT  
 CATATACTTATTTTATTTTTTCCATAATCTTATAGCACTGCATCGTTATTAAGCCCTTAT  
 TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA  
 GTTTCTAAAGCCAAGAAGATTTATTACAAATCAGAATCTTGGAGGCAAAATCTTCTGCGAT  
 ACCAAAGTGATAAATCTCTGTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT  
 CTGTGTTGCTTTGAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
 AACCAACTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAAACT  
 ACCTTTTTGTTCCCCACTTAAATGTATTGTTTCCCAAGTGTAATTATCATGCGTGTTTA  
 TATCTTCTTAATAAGGTGTGCTGTGTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
 ATCTGGTGACAAATATTTCTCTGTAGCTGTAAAGCAAGTCACTTAATCTTTCTACCTTTTT  
 TTCTATCTGCCAAATTGAGATAATGATACTTAAACAGTTAGAAGAGGTAGTGTGAATATTAA  
 TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCTTATGATGTCTTTATTGTCT  
 CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
 CACTGCCTTCTCTCTTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
 GTGGTTCACTGCTCTTCTCTCTTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
 CTTCACTGTGGCTCAGTGCTCTCTCTCTTACCAGTCTATTTCCATTCTTCAGCTGTGCT  
 GACATTTTGTGCTGCTGTTCATTTTAAACAATGCTCTTACTTTTCCAGTCTGTGACAGAAT  
 CTATTTCATCTGAGCAAGATGTAAATGAAAGGGTGTGGCATGGGTCTGGAGCACTG  
 GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGGAGCAAGGCATTGGCTGCTGTAA  
 GCTTATTGCTTCACTGTAAAGCGGTGGTTTGTAACTCTGATCTTCCACCTCACAGTGATG  
 TTGTGGGATCCAGTGAGATAGAATACATGTAAGTGTGTTTGTAAATTAAGAAAGTGCTAT  
 ACTAAGGGAAGAAATTGAGGAATTAAGTGATACGTTTTGTGTGTGCTTTTCAAATGTTTGA  
 AAATAAAAAAATGTTAAG

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## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI~~L~~AWIGAI~~V~~STALPQWRIYSYAGDNIVTAQAMYEG~~L~~WMSCV~~S~~QSTGQI  
QCKVFD~~S~~LLNL~~S~~STLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDD~~E~~VQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMT~~P~~VNARYEFGQALFTGWAAASLCLLGGALLCCSC  
PRKTT~~S~~YPTPRPYPKPAPSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

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